Human Biogeography: Comparative Phylogeography of Modern Humans and Other Organisms

Aims and Rationale - We will compare the published phylogeographies (genetic biogeographies) of modern humans with those of other vertebrates to elucidate the patterns of population movement in the past. The science of phylogeography provides an understanding of the population dynamics of species in relation to landscape, climate and human related processes over the last 50 thousand years. Species respond to these processes individually, for example using different refugia at different times. The location of these refugia is also determined by the geography and topography of the landscape. Phylogeography can be used to identify the location of these species refugia and/or the place of origin of domestic / commensal species. Methods - Phylogeographic studies have been performed on organisms as varied as red deer, trout, snails, oak trees, ferns and bacterial and viral pathogens like Black Death and Rabies. Studies have also been done on domestic (sheep, cattle, wheat) and commensal (house mouse, black rat) plants and animals. The data from most of these studies are deposited on GenBank (a freely accessible online database). The project will analyse such data to look at the various patterns seen in each species which can then be grouped by similarity according to geographical and genetic diversity indices. These will include the likely divergence dates of the diversity as well as the topology of the species' phylogenetic tree or network diagrams. The data will also be analysed using GIS and associated geospacial statistics to help identify the place of origin and source of spread of populations. Hypotheses: Human phylogeographic patterns in Europe that relate to Upper Palaeolithic distribution change will generally have a North/South distribution similar to wild species coming out of ice age climate refugia. Those patterns with an East/West distribution will be similar to taxa whose climate refugia was in the East (or South East) or to that of domestic/commensal plants and animals whose origins lay in the South East, representing Neolithic or later distribution change. Clearly defined outputs - The outputs would include a paper submitted to a high impact journal (Nature, Science, PNAS) summarising the general results of the project. A further three papers are envisaged in subject specific journals like Molecular Ecology, Journal of Human Evolution and the Journal of Biogeography. The results of the work will also be presented at international meetings such as that of the Society of Molecular Biology and Evolution, the European Society of Human Evolution etc. Academic Impact Stewart's paper in Science which looks at Late Pleistocene Humans outside of Africa in relation to the biogeographical patterns of other organisms suggests that there would be an appetite amongst the people in the human evolution community for such an analysis. The research will have an impact on biological anthropology (human evolution), biogeography and molecular ecology thanks to the production of a minimum of 4 publications as well as the participation at international conferences (see above). The evolution and population genetics (phylogeography) of humans receives a disproportionate amount of attention. Other organisms, although they do not receive the same depth of attention as humans represent the breadth of possible patterns and corresponding processes that can exist in organisms over these time scales. Comparing the genetic patterns in humans with those in other organisms will help identify similarities and differences between them. The ecological and general biological characteristics of similar and differing species' patterns will help reduce the possible explanations for those patterns. For example humans are widespread geographically similar to wolves, ravens and pike but their phylogeographic patterns are different which may be driven

by different limitations on their dispersals or the length of time since dispersal. Societal Impact The evolution of humans receives a lot of media coverage and Stewart is regularly interviewed by the media on this topic, both relating to his own research and that of other scientists (e.g. New Scientist, BBC World Service). The response of organisms to climate change is also of great interest to the public and receives a corresponding amount of media attention in light of current climatic changes and species' range shifts. The proposed project will undoubtedly have a significant impact due to the public interest it generates. The understanding of population dynamics in species is important to future conservation of biotas, so the proposed project will have an important contribution to make to conservation planning. Stewart was involved in a Natural England consultancy project looking at the identification of future climate refugia and guide strategy. The proposed project will enhance the likelihood of the supervisory team, as well as the PhD student, being involved in such initiatives in the future which seem to be increasingly on the agenda of NDPDs (Natural England) and NGOs (RSPB) and which will likely influence UK government policy-makers. Such project will have the potential to be used as case impact for the REF2020. Training Opportunities The student will come away from this project with a unique skill set that bridges a number of important fields in modern day science such as biogeography, molecular ecology as well as human evolution. 1) The student will get training in performing analysis of molecular data (tree and network construction, BEAST etc.) as well as innovative meta-analytical methods developed by Stewart and Hardouin to analyse data from GenBank. The student will be trained in laboratory techniques used in analyses such as PCR, sequencing, electrophoresis and will likely take part in house mouse phylogeographic analyses (Hardouin). There will also be an opportunity for aDNA training with Richards in Huddersfiled University in his Leverhulm Trust funded Doctoral Scholarship Centre in Evolutionary Genomics. 2) The student will be trained in the essential tools of modern biogeography and conservation: statistical techniques and GIS methods for exploring species' responses to climatic and anthropogenic changes (Stafford). 3) The student will also receive training in relevant human evolutionary science SUPERVISORY TEAM First Supervisor Dr John Stewart Additional Supervisors Emilie Hardouin Rick Stafford External Supervisor: Prof. Martin Richards, Huddersfiled University Recent publications by supervisors relevant to this project Stewart, J.R. and Stringer, C. B., 2012. Human Evolution Out of Africa: The Role of Refugia and Climate Change. Science, 335 (6074), 1317-1321. (IF- 31.48). Brace, S.; Palkopoulou, E.; Dalďż˝n, L.; Lister, .M.; Miller, R. ; Otte, M. ; Germonprďż˝, M.; Blockley, S.P.E. ; Stewart, J.R. & Barnes, I. 2012. Serial population extinctions in a small mammal indicate Late Pleistocene ecosystem instability. Proceedings of the National Academy of Sciences 109(50): 20532-6. (IF: 9.809). Lagerholm, V.K., Sandoval-Castellanos, E., Ehrich, D., Abramson, N.I., Nadachowski, A., Kalthoff, D.K., Germonprďż˝, M., Angerbjďż˝rn, A., Stewart, J.R., Dalďż˝n, L. 2014. On the origin of the Norwegian lemming. Molecular Ecology. doi:10.1111/mec.12698 (IF: 5.52). Stewart, J.R., Barnes, I., Lister, A.M. and Dalďż˝n, L. 2010. Refugia Revisited: Individualistic responses in space and time. Proc. Roy. Soc. B. 277: 661 - 671. (IF: 5.683). Hardouin EA, Orth A, Teschke M, Tautz D, Bonhomme F: Worldwide mouse differentiation at microsatellite loci identifies the Iranian plateau as a phylogeographic hotspot. Accepted in BMC Evolutionary Biology (IF: 3.41). Hardouin EA, Tautz D: High mitochondrial mutation rates after an island colonization event - selection or near-neutrality? Biology Letters 2013, doi: 10.1098/rsbl.2012.1123. (IF: 3.35) Linnenbrink M, Wang J, Hardouin EA, Kďż˝nzel K, Metzler D, Baines JF: The role of biogeography in shaping diversity of the intestinal microbiota in

house mice. Molecular Ecology 2013, doi: 10.1111/mec.12206. (IF: 5.52). Myles S, Lea AR, Ohashi J, Chambers KG, Weiss GJ, Hardouin E, Engelken J, Macartney-Coxson PD, Eccles AD, Naka I, Kimura R, Inaoka T, Matsumura Y, Stoneking M: Testing the thrifty gene hypothesis: the Gly482Ser variant in PPARGC1A is associated with BMI in Tongans. BMC Medical Genetics 2011, 12:10doi:10.1186/1471-2350-12-10. (IF: 2.33). Stafford R., Smith V.A., Husmeier D. Grima T. and Guinn B. 2013. Predicting ecological regime shift under climate change: new modelling and molecular-based approaches. Current Zoology. 59: 403-417. (F: 1.81) Stafford R., Goodenough A.E. and Hart A.G. 2013. A visual method to identify significant latitudinal changes in species' distributions. Ecological Informatics.15: 74-84. (IF: 1.980) Pala, M., Olivieri, A., Achilli, A., Accetturo, M., Metspalu, E., Reidla, M., Tamm, E., Karmin, M., Reisberg, T., Hooshiar Kashani, B., Perego, U.A., Carossa, V., Gandini, F., Pereira, J.B., Soares, P., Angerhofer, N., Rychkov, S., Al-Zahery, N., Carelli, V., Sanati, M.H., Houshmand, M., Hatina, J., Macaulay, V., Pereira, L., Woodward, S.R., Davies, W., Gamble, C., Baird, D., Semino, O., Villems, R., Torroni, A., Richards, M.B. (2012). Mitochondrial DNA signals of Late Glacial re-colonisation of Europe from Near Eastern refugia. The American Journal of Human Genetics 90: 915-924. (IF: 10.987) Mellars, P., Gori, K., Carr, M., Soares, P., Richards M.B. (2013) Genetic and archaeological perspectives on the initial modern human colonization of southern Asia. Proc. Natl. Acad. Sci. USA 110:10699-10704. (IF: 9.809) Costa, M.D., Pereira, J.B., Pala, M., Fernandes, V., Olivieri, A., Achilli, A., Perego, U., Rychkov, Y., Naumova, O., Hatina, J., Woodward, S.R., Eng, S., Macaulay, V., Carr, M., Soares, P., Pereira L., Richards, M.B. (2013) A substantial prehistoric European ancestry amongst Ashkenazi maternal lineages. Nature Communications, 4: 2543. (IF: 10.742) INFORMAL ENQUIRIES Please feel free to contact John Stewart via email - jstewart@bournemouth.ac.uk for queries related to the research project. ELIGBILITY CRITERIA All candidates must satisfy the University's minimum doctoral entry criteria for studentships of an honours degree at Upper Second Class (2:1) and/or an appropriate Masters degree. An IELTS (Academic) score of 6.5 minimum (or PhD Studentship Project Description March 2015 equivalent) is essential for candidates for whom English is not their first language The ideal candidate should have GIS skills, quantitative ecological modelling skills and field research skills and an MSc/ MRes degree in a related field. This project requires somebody who is confident in working in an African Savannah habitat and has the maturity to deal with field work under sometimes difficult conditions, to manage a research project if required, and who can work independently in the field. Field work experience will therefore be expected. HOW TO APPLY Please complete the BU Research Degree Application 2015 and submit it via email to the Postgraduate Research Administrator for Admissions Suzy Kempinski - pgradmissions@bournemouth.ac.uk

by 1 May 2015

. Further information on the application process can be found at www.bournemouth.ac.uk/phd-2015

Dr. Emilie Hardouin Associate lecturer in Conservation Genetics Bournemouth University Faculty of Science and Technology Christchurch House Talbot Campus Poole, Dorset BH12 5BB United Kingdom Tel: +0044 (0)1202 962402 BU is a Disability Two Ticks Employer and has signed up to the Mindful Employer charter. Information about the accessibility of University buildings can be found on the BU DisabledGo webpages This email is intended only for the person to whom it is addressed and may contain confidential information. If you have

 Emilie Hardouin <
ehardouin@bournemouth.ac.uk
>